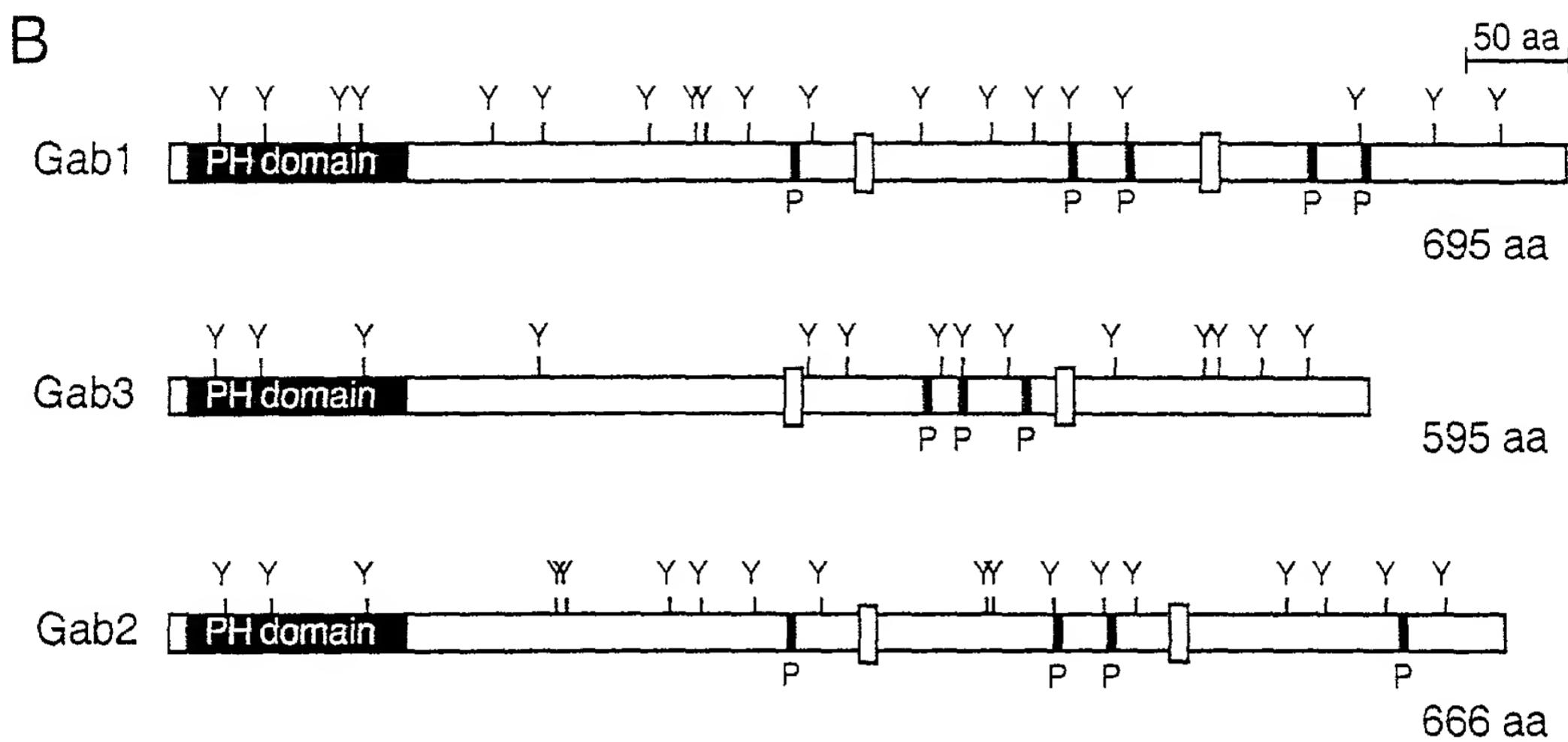


A

Human	MSAGDAVCTGWLVKSPPERKLQRYAWRKRFVLRRGRMSGNPDVLEYYRNKHSSKPIRVI	60
Murine	MSTGDTVCMGWLKSPPERKLQRYAWRKRFVLRRGRMSGNPDVLEYYRNKHSNKPIRVI	60
	::*** ***:*****:*****:*****:*****:*****:*****:*****:*****	
Human	DLSECAYWKHVGPSFVRKEFQNNFVFIVKTTSRFYLVAKTEQEMQVWVHSISQVCNLGH	120
Murine	DLSECTVWKHAGPGFIRKEFQKNFVFIVKTTSRFYLVAKTEEMQVWVHSISQVCNFSH	120
	*****:*****.***.*:*****:*****:*****:*****:*****:*****:..*	
Human	LEDGADSMESLSYTPSSLQPSASSLLTAHAASSSLPRDDPNTNAVATEETRSEELLFL	180
Murine	LEDGADSMESLSHMPSSFQPSPASSLHTVHVANSALLKDDGNTNSVVTETRRESEFLFL	180
	*****:*****: ***:***.*** *.*.*.*: * :** ***:*.***** ***:***	
Human	PDYLVLSNCETGRLHHTSLPTRCDSWSNSDRSLEQASFDDVFDCLQPLPSSHVLVHPSCH	240
Murine	PDYLILSNCETGRLHASL PTRCDSWSNSHSLAQTSFDDVFLDGLQPFISNNLVHPLHH	240
	*****:*****:*****:*****:*****:*** *:*****:***:***: * ..:*** * *	
Human	GSGAQEVPSRPQAALIWSREINGPPRDHLSSPLLESSLSSTIQVDKNQGSLPCGAKEL	300
Murine	GKVSQDFPSIRPQASLIWNREINGPSRNLMSSPLLESSLNPTVHVEEKQVSLPSGVKEL	300
	. ::..** ****:***.*****.*: :*****:*****..*:***:***:***.***	
Human	DIMSNT[PPRPPKPSHL]SERRQEE--WSTHSGSKKPECTLVPRRISLSGLDNMRTWKADV	358
Murine	NIMSNI[PPRPPKPSYL]SEQRQDQPLLTGHSSNKKPGYTMVPRRISLSGLDHGVSWKGDV	360
	:***** *****:***:***: : * ..*** *:*****:*****: :***.**	
Human	EGQSLRHRDKRLSLNLPCRFSP[MYPTASASIEDSYVPMSE]QAGASGLGPHCSPDDYIPMN	418
Murine	QSQSLRHRDKRLSLNLPCFKFSPIYPTASPSAEDSYVPMSE[KGTASELRPHCSQDDYIPMS]	420
	:.*****:*****:***:*****.* *****:.. ** * *** *****.	
Human	SGSISSPLPELPANLE[PPVNRDLK]QRKSRPPLDLRNLSIIREHASLTRTRTVPCSRT	478
Murine	S----SMLPELPADLE[PPVNRNLK]QRKSRPPLDLSRNLSI[QH]EHTSLTRTYVPCNRT	476
	* * *****:*****:*****:*****:***** * :***:***** ***.**	
Human	SFLSPERNGINSARFFANPVSREDEES-----YIEMEEHRTASSLSSGALTWTK	527
Murine	SFLSPQRNGINCARLFSTPSEEEEEEEEEEKYIQMEEYGTVSSLRSALSWK	536
	*****:*****.**:*** ..*:***. ***:***: * .*** .**:***	
Human	<u>SHP2</u>	
Murine	KFSLDYLA[DFNSASPAPMQQKLL]SEEQRVDYVQVDEQKTQALQSTKQEWTDERQSKV	586
	KFSLDYLA[DFNSTSPAPVQKKLL]SEEQRVDYVQVDEQKTQAFRSTKQAWTDERQSKV	595
	*****:*****:*****:*****:*****:*****:*****:*****:*****	

Figure 1A



C

Gab3	MSTG--D-TVCMGWLIKSPPERKLQRYAWRKRWFVLRRGR	37
Gab2	MSGGGGGDDVVCTGWLRLKSPPEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VVCSGWLRLKSPPEKKLKRYAWKRRWFVLRSGR	37
	*** * : .** *** * ****: * : * ***: : * ***: * * **	
Gab3	MSGNPDVLEYYRNKHSNKPIRVIDLSECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYYKNEHSKKPLRIINLNLCQVD-AGLTFNK	79
Gab1	LTGDPDVLEYYKNDHAKKPIRIIDLNLNCQQVD-AGLTFNK	76
	: : * : * **** * : * . * : : * : * : * . * . * * * : * :	
Gab3	KEFQKNFVFIVKTTSRIFYLVAKTEEEMQWVHSISQVCN	117
Gab2	KELQDSFVFDIKTSERTFYLVAETEADMNKWVQSICQICG	119
Gab1	KEFENSYIFDINTIDRIFYLVADEEDMNKWVRCICDICG	116
	***: . . : * : * . * * * * . : * : * : * : . * . : * .	

Figure 1B and C